

FIGURE 1

TNIK 1 MASDSEPARSLDTIDLSLRLDFACIFELVELVGNGTYGQVXKGKHVKTCGIAAIKVMDVTCDEEERIKOETNMIKKYSHHR
 NIK 1 MANDSEAKSLVDTIDLSLRLDFACIFELVFGVNGNTYGQVXKGKHVKTCGIAAIKVMDVTCDEEERAVTCINMIKKYSHHR

 TNIK 81 HIATYYGAFIKKNEPECDEQIWLVUMFCCAGSITDIKNTKGNTLKEEWIAPICREILRCISHLHCKVTHRIVTRGQNVL
 NIK 80 HIATYYGAFIKKSPEGMODQLWLVUMFCCAGSITDIKNTKGNTLKEEWIAPICREILRCISHLHCKVTHRIVTRGQNVL

 TNIK 161 LTENAEVKLVDFGVSAQDLRTVGRNNTFTCTPYWMAPEVIACDENPATATYDQEDLWSGITAIFMAECAPPICMMHPMC
 NIK 160 LTENAEVKLVDFGVSAQDLRTVGRNNTFTCTPYWMAPEVIACDENPATATYDQEDLWSGITAIFMAECAPPICMMHPMC

 TNIK 241 ALFLIPRNPAKIKKEKKWSKKFSEPIESCLVKNHEQRPATEQIMKHPITRDQPNERQVRQLKDHTDKKKGEKIETE
 NIK 240 ALFLIPRNPAKIKKEKKWSKKFSEPIESCLVKNYQKPISTEQIMKHPITRDQPNERQVRQLKDHTDKKKGEKIETE

 TNIK 321 YEYSGSEEEERN--DSGERSSILNPGESTLRRDFLRLOOENKERSEALRKQOLQO--RENEEHRIQOLLAEEROKRTE
 NIK 320 YEYSGSEEEERPVPEOPCPSSILNPGESTLRRDFLRLOOENKERSEALRKQOLQO--RENEEHRIQOLLAEEROKRTE

 TNIK 397 EKEQKRRLEEQQIREKEKREQQEREORK-----KMEEDOKR--EEFRNAEHEQEYIKNQLEEEQHQLE
 NIK 400 QKEQKRRLEEQQIREKEKREQQEREORKREKEKRRLEELERKKEEDERRAGEEKKVERMQYIKNQLEEEQHQLE

 TNIK 460 ILGCOLLHEQAMLLYKROLEPQAEQFQSKQERDYLVLSQLHQREQRPVEKNNLYHYKEGMSESEKEPAWKEVPC
 NIK 480 ILGCOLLHEQAMLLHDHRPHAQDPPPFQDQNS-----KPSHAPC--PK--HYOPAD

 TNIK 540 RSTLNQHSPAMPIKVNANRISDPHPERSEPSISGVOPARTPMINPVQDQPHLVAVKSQGPALTASQSVHEQPNGL
 NIK 532 NAEVOWS---HLASIKN---NVSPVSRHSBDSPLKFARRHLRSODECEP--SR---SECI

 TNIK 620 SGFOCALNVTSHRVEMPRONSDPTSENPELPTRISKEDRSSWLRQEM--TPVVECITTSISPLARKNSPCNGSALGPR
 NIK 584 S-----SSSDSKSE-VPEP-----OKAWSRSDSDEVPERVEVTTSRSPVLEKRD51126GCOONS

 TNIK 699 L-CSDPIRASNPDLRTEPILESPVOKTSC9S9S9TSSQPSQEGSOPCSLAGSEMINRVKANEKSEGSPVLPHPAK
 NIK 640 QCGRNSTSSEPPILMVERVEKUVERPC9CS9S9S9NAGSOP---GSHEC9S9GCHKURV9SSKSEGSPSPROSAA

 TNIK 779 VKEPERSDTTPSRPASYKKALDULATALAKELNRDIEBTNMKVKVTDYSSSEEDSSEBBEMICSEETHIGTVAVS
 NIK 716 KNPDDKKEVBR---SLKFACEVULATALAKELNAV---EDVKEPPEHVTDYSSSEEDCTDDEBZDVMQEGADDSTSGP

 TNIK 859 DIFKLIFCAPCSNEQYNVGVGTIIGLETSHADSFSC3ISYEGTLMIRETSGERKRSCHD9NGFAGHINLPDLVOCHE
 NIK 788 DOTRAASSPNLNGETSVKTVIVIDVSEP---AMFESKEGLTVKTOBASS-----TIEKIK

 TNIK 939 PAGTPTEGLGRVSTHSQEMDSCTEYGHGSSTKAEGTFPVNPHMIGTSIADDEDEEESAAALPSPVTCQDQAKLNAR
 NIK 846 -----SSSEFTDQDQKLIWISI9S6---GTVTAEVVCPSCDCLKPEAIRODPT

 TNIK 1019 KISVVVNVNPTNIREHSDTPEIIRKYKKRFNSEILCAALWGVNLIIVC7TMSHMLDRSGQGKVYDILMRKRYDMVLEGIN
 NIK 892 KGSVVVNVNPTNIREHSDTPEIIRKYKKRFNSEILCAALWGVNLIIVC7TMSHMLDRSGQGKVYDILMRKRYDMVLEGIN

 TNIK 1099 VLVTISGKICLKVYYLAWLKNRILHNDPEVEKKQCMITVGDILEGGCHYKVVKYERIKPVIVIAIKNAVEYAWAPKTYHK
 NIK 972 VLVTISGKICLKVYYLAWLKNRILHNDPEVEKKQCMITVGDILEGGCHYKVVKYERIKPVIVIAIKNAVEYAWAPKTYHK

 TNIK 1179 EMFKSEFADLQKPLLVLTVVEEGORLKVIQGSHTGFHIVDVSSEYDIXTSHICGHTPHAINLICLTDGMEMLVCY
 NIK 1052 EAFFKSEFADLQKPLLVLTVVEEGORLKVIQGSCTGFHIVDVSSEYDIXTSHICGHTPHAINLICLTDGMEMLVCY

 TNIK 1259 EDEGVVYNTYCRITKDVVLOWGEMPTSVAIYH9NCMGWGEKAIEIRSVETGILDCVEMMKHAQNLKEFCRNLKVKDFAS
 NIK 1132 EDEGVVYNTYCRITKDVVLOWGEMPTSVAIYH9NCMGWGEKAIEIRSVETGILDCVEMMKHAQNLKEFCRNLKVKDFAS

 TNIK 1339 VRSGGSSQVLMPIANNBMMNW
 NIK 1212 VRSGGSSQVEMTICMBSLW

FIGURE 2

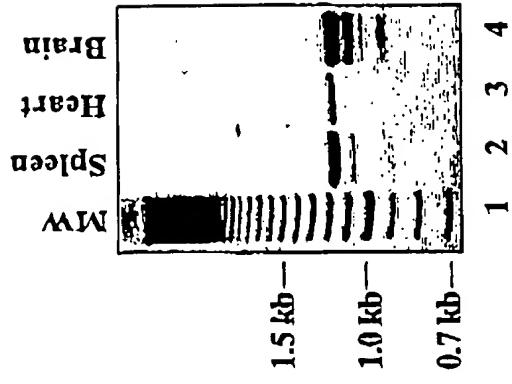


FIGURE 3

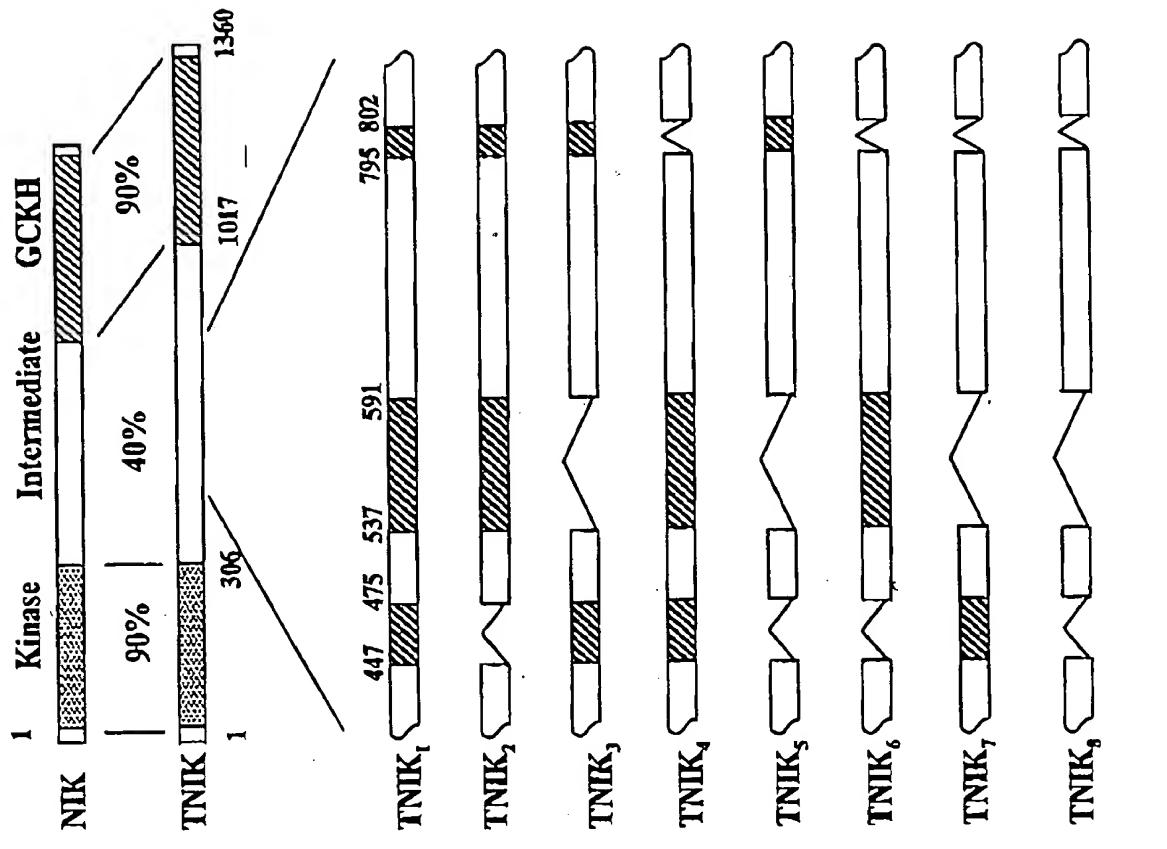


FIGURE 4

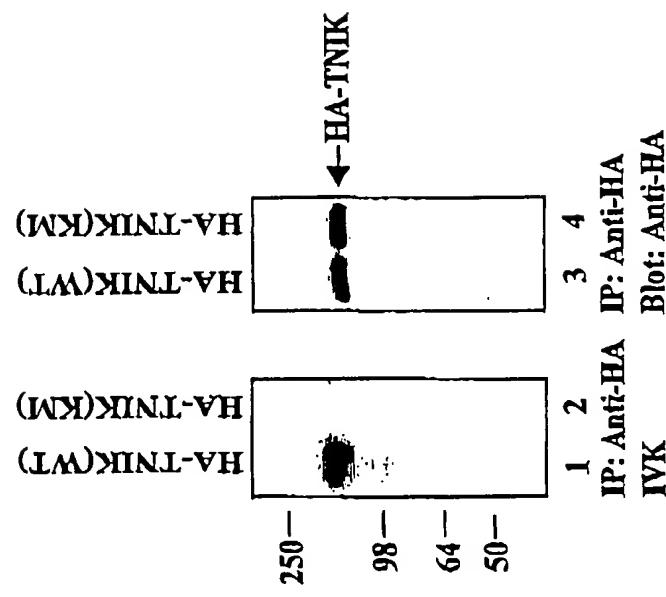
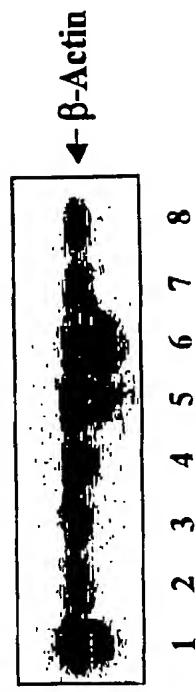


FIGURE 5B



1 2 3 4 5 6 7 8

FIGURE 5A

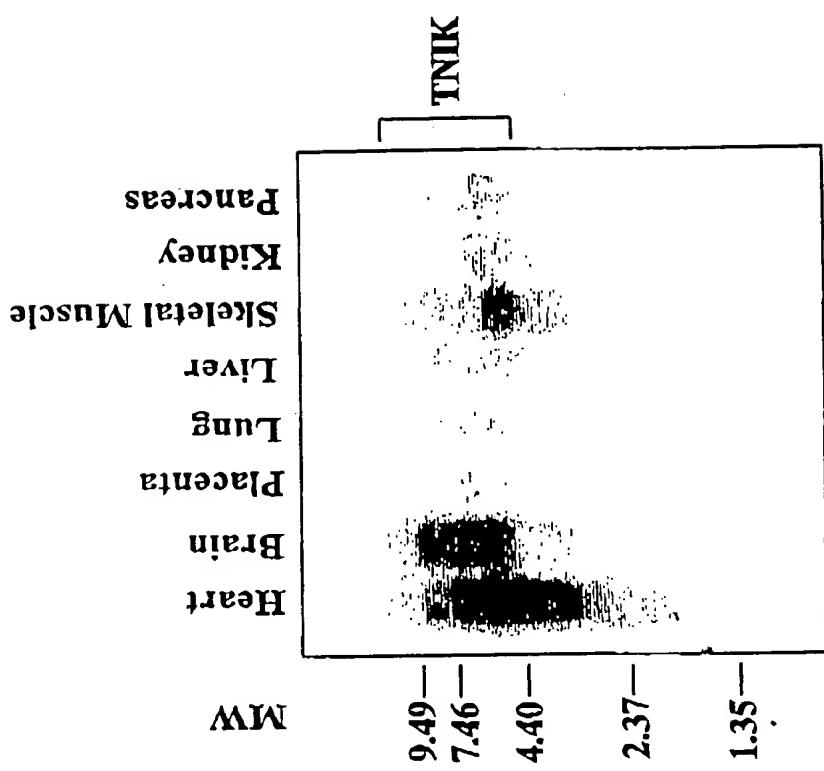


FIGURE 6

Transfection:
Vector
HA-TNIK

IP: Anti-HA
Blot: Anti-Traf2 64
← Traf2
98
50
36

Lysate
Blot: Anti-HA
← HA-TNIK
1 2

Lysate
Blot: Anti-Traf2
← Traf2
1 2

Lysate
Blot: Anti-HA
← HA-TNIK mutants
1 2 3 4 5 6

Transfection:
TNIK(WT) HA¹
Kinase 306 Intermediate 1017 GCKH 1360
TNIK(N1)
TNIK(N2)
TNIK(C1)
TNIK(C2)
TNIK(M)

HA-TNIK mutants
E Z Z S S K
Transfection:
IP: Anti-HA
Blot: Anti-FLAG
← FLAG-Traf2

FLAG-Traf2
E Z Z S S K
Transfection:
IP: Anti-HA
Blot: Anti-FLAG
← FLAG-Traf2

FLAG-Traf2
HA-TNIK mutants
1 2 3 4 5 6
Transfection:
IP: Anti-HA
Blot: Anti-FLAG
← FLAG-Traf2

FIGURE 7

Figure 8A

Figure 8B

Figure 8C

HA-TNIK
mutants

FIGURE 9

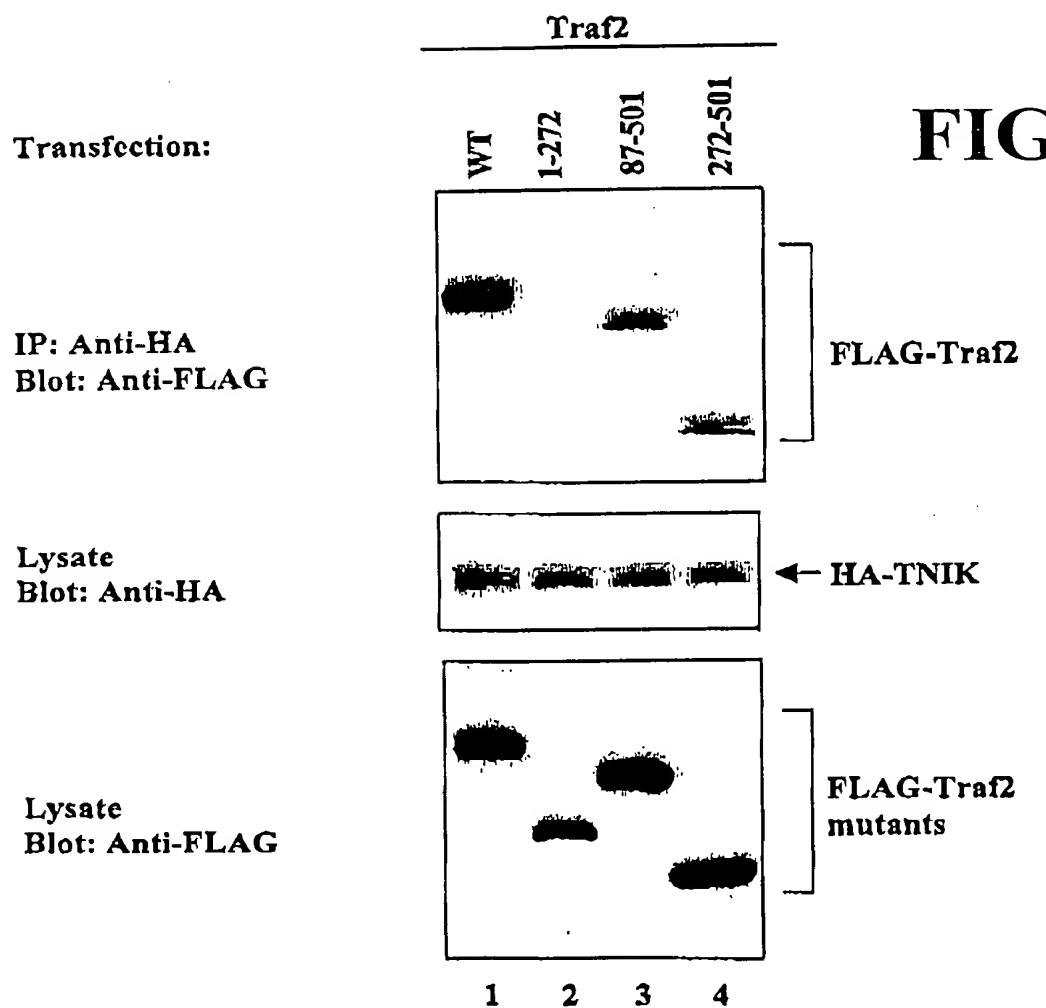
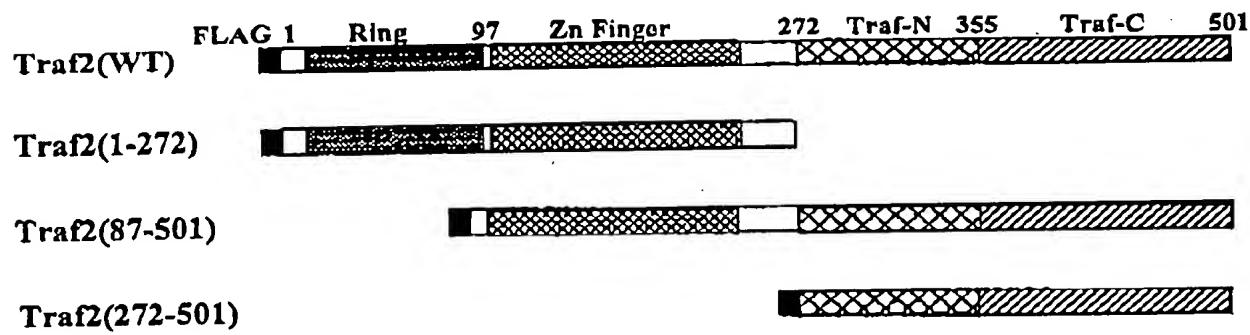


FIGURE 10

FIGURE 11

B.

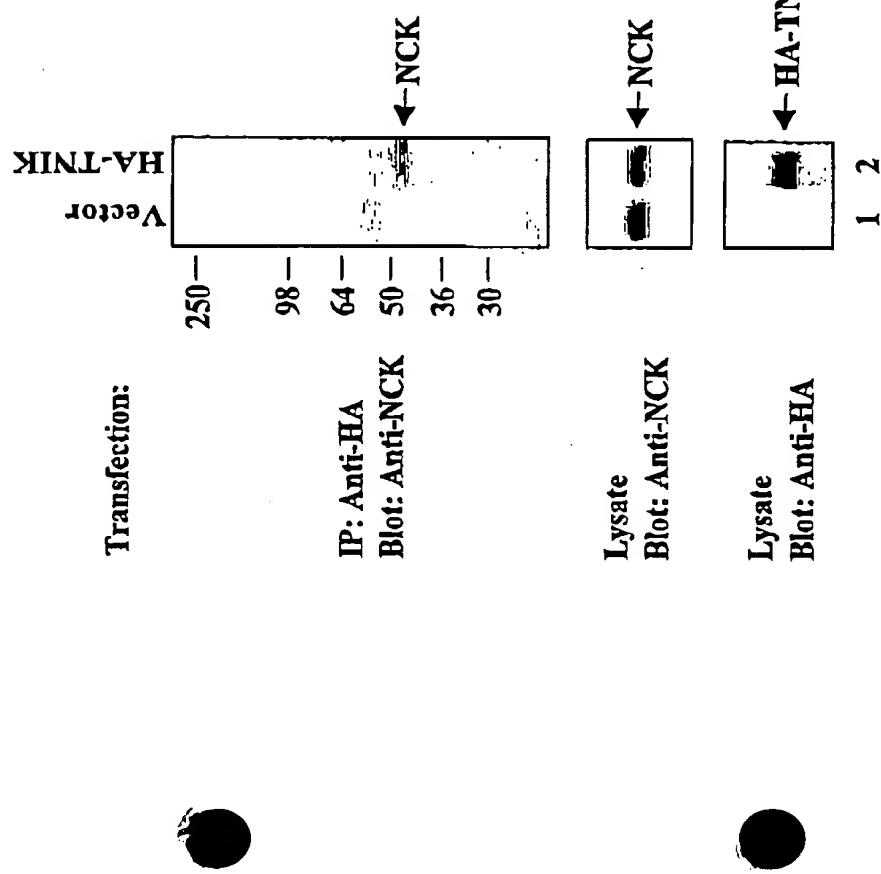


FIGURE 12

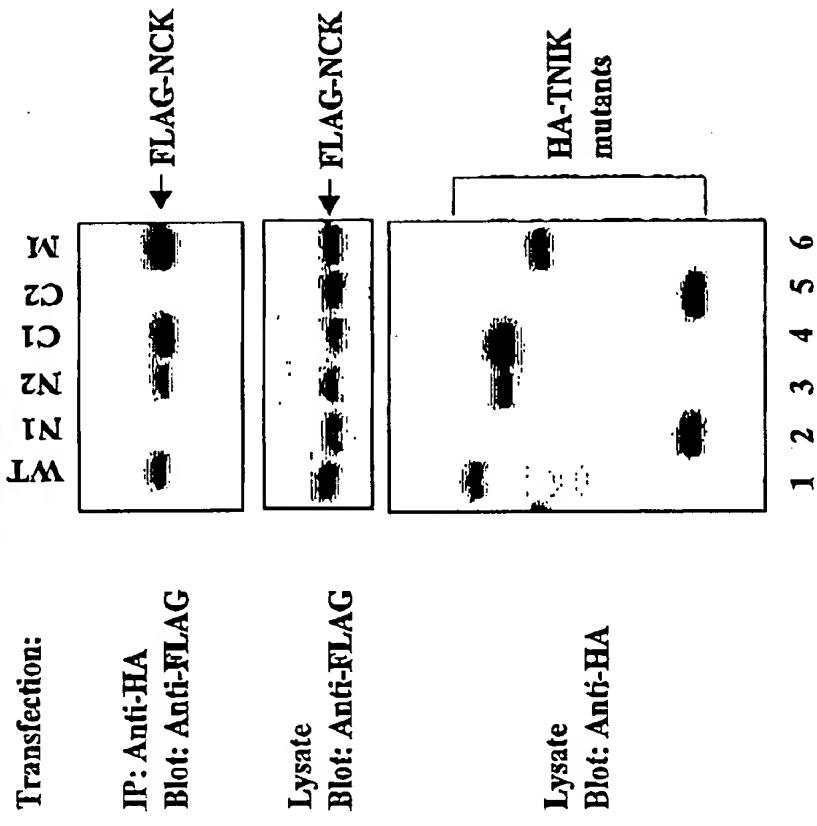
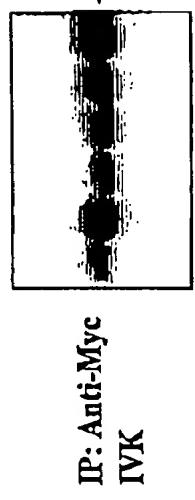


FIGURE 13

FIGURE 15

Transfection: Vector HA-TNIK Traf2

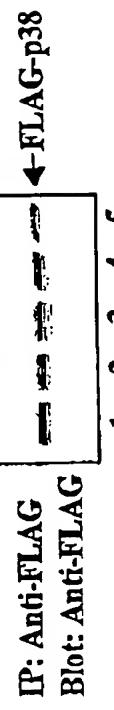
(μ g)	1	2	3	1	-	-	-
TNIK:	-	+	-	-	-	-	-



1 2 3 4 5 6

Transfection: Vector HA-TNIK MEKK1

(μ g)	1	2	3	0.05	-	-	-
MEKK1:	-	+	-	-	-	-	-



1 2 3 4 5

B.

Transfection: Vector HA-TNIK MEKK1

(μ g)	1	2	3	0.05	-	-	-
MEKK1:	-	+	-	-	-	-	-



1 2 3 4 5

D.

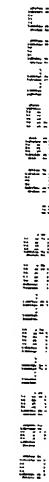
Transfection: Vector HA-TNIK mutants

	WT	K22Z	S25Z	M28S	MEKK1	-	-
TNF:	-	+	-	-	-	-	-

1 2 3 4 5 6 7 8 9 10

FIGURE 14

FIGURE 16



A.

Vector



TNIK



TNIK(KM)



TNIK(N1)



TNIK(C1)



JNK2



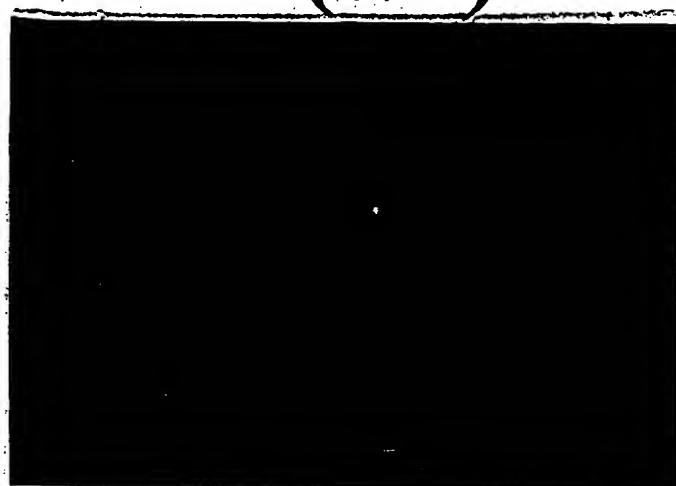
FIGURE 17

FIGURE 18

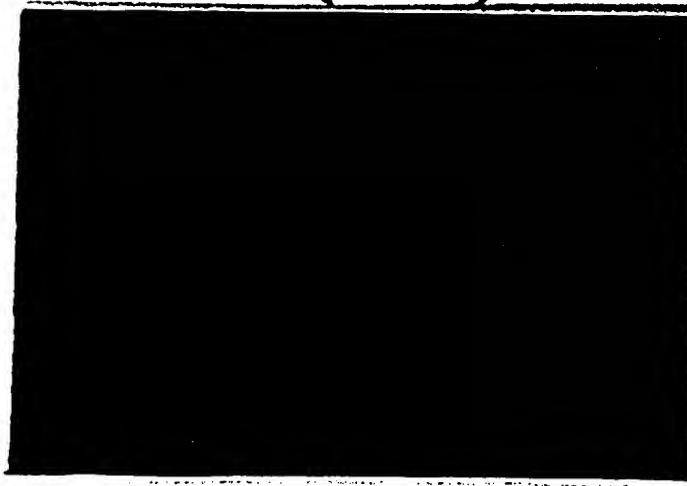
Vector



TNIK(WT)



TNIK(KM)



RIP



FIGURE 19

FIGURE 20

D.

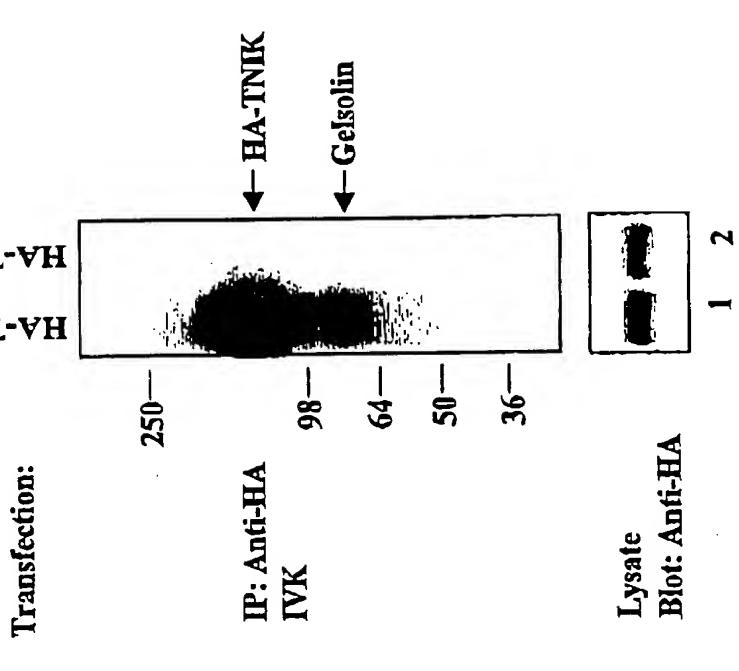
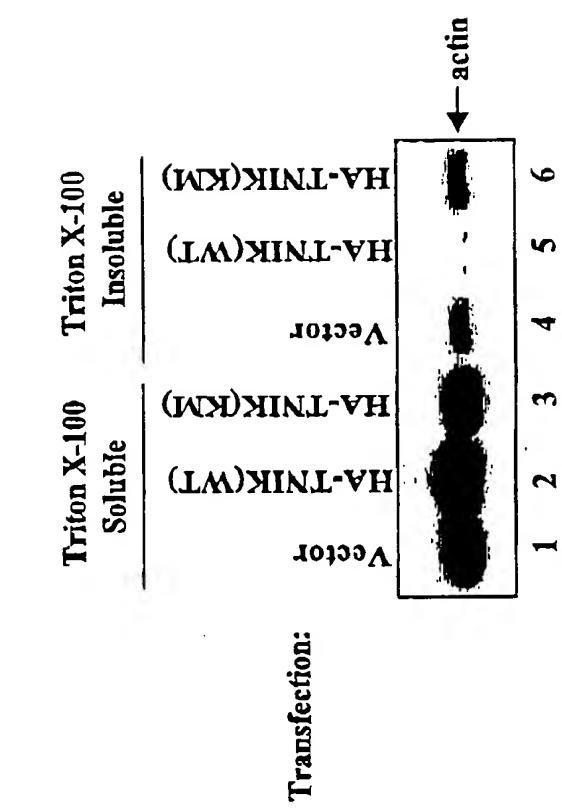


Figure 21

ATGGCGAGCAGCTCCCCGGCTCGAAGCCTGGATGAAATAGATCTCTCGGCTCTGAGGGACCCCTGCAGGGATCTT
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TATTCTCATCACCGGAATATTGCTACATACTATGGTCTTTATCAAAAAGAACCCACCAGGCATGGATGACCAA
CTTGGGTGGTGGAGTTGTGGCTGGCTCTGTCACCGACCTGATCAAGAACACAAAAGGTAACACGTTG
AAAGAGGAGTGGATTGCATACATCTCAGGGAAATCTACGGGGCTGAGTCACCTGCACCGCATAAAGTGATT
CATCGAGATATTAAAGGGCAAAATGTTGACTGAAATGAGAAGTTAAACTAGTGGACTTGGAGTCAGT
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GCCTGTGATGAAAACCCAGATGCCACATATGATTTCAAGAGTGACTTGTGGTCTTGGTATCACCAGCATTGAA
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CCTCGGCTGAAGTCTAAGAAGTGGTAAAAAAATTCCAGTCATTTATTGAGAGCTGTTGGTAAAGAATCACAGC
CAGCGACCAGCAACAGAACATTGATGAAGCATTACGAGACCAACCTAATGAGCAGCAGGTCCGCATT
CAACTCAAGGACCATATTGATAGAACAAAGAACAGAGCAGGGAGAAAAAGATGAGACAGAGTATGAGTACAGTGG
AGTGAGGAAGAACAGGAGGAATGACTCAGGAGAGCCCAGCTCCATCCTGAATCTGCAGGGAGTCAGCCTG
CGGAGGGACTTCTGAGGCTGCAGCTGCCAACAGGAGCCTGAGGCCCTACGGAGGCAGCAGCTGGAGCAG
CAGCAGCGGAGAACATGAGGAGCACAAGCGCAGCTGGCCGAGCGTCAGAACAGCAGTCAGGGAGCAGAACAG
CAGAGCGGGCGGCTGGAGGAGCAACAAAGCGAGAGAACAGGAGCTGGGAAGCAGCAGGGAGAGGAGCAGCG
CACTATGAGGAGCAGATGCGCCGGAGGAGGAGGAGGAGGAGGCGTGCAGCATGAAACAGGAATACATCAGGCACAG
TTAGAGGAGGAGCAGAGACAGTTAGAGATCTTGACAGCAGCTACTGCATGAAACAGCTACTTCTGGAAATAT
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CAGGGACCTGCCTTGACGCCCTCCAGTCAGTGACGAGCAGCCCACAAAGGGCTCTGGGTTTCAGGAGGCT
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GGAACCTTGATGATTAGAGAGACGTCAGGAGAGAACAGCAGTCAGGAGACCTGGGACTGGGAGCAGCACCAAGC
CACATCAACCTCCCTGACCTGGTCAGCAGAGCCATTCTCAGCTGGAAACCCGACTGAGGGACTGGGCGCGTC
TCAACCCATTCCAGGAGATGGACTCTGGACTGAATATGGCATGGGAGCAGCACCAAGCCTCTTCAACCCCC
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GACCCAGAAGTAGAAAAGAACAGGCTGGATCACTGTTGGGACTTGGAAAGGCTGTATACATTATAAGTGT
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GTGCTTCAATGGGAGAAATGCCACAGTCAGTGGCCTACATTCAACTCAGATAATGGCTGGGCGAGAAA
GCTATTGAGATCCGGTCAGTGGAAACAGGACATTGGATGGAGTATTGTCATGCTAAAGCAGCTCAAAGGTTAAAG
TTTCTATGTGAAAGAAATGATAAGGTATTTTGACATCCGTGCGATCTGGAGGAAGTAGCCAAGTGTGTTTCTG
ACCCCTCAACAGAAATTCCATGATGAACTGGTAA

Figure 22

ATGGCGAGCGACTCCCCGGCTCGAAGCCTGGATGAAATAGATCTCTCGGCTCTGAGGGACCCCTGCAGGGATCTT
GAATTGGTGGAACTTGTGGAAATGGAACATACGGGCAAGTTATAAGGGTCGTATGTCAAAACGGGCCAGCTT
GCAGCCATCAAGGTTATGGATGTCACAGGGATGAAGAGGAAGAAATCAAACAAGAAATTACATGTTGAAGAAA
TATTCTCATCACCGGAATATTGCTACATACATGGTCTTATCAAAAGAACCCACCAGGCATGGATGACCAA
CTTGTTGGTGTGAGTTGTGGTGTGGCTCTGTCACCGACCTGATCAAGAACACAAAAGTAACACGTTG
AAAGAGGACTGGATTGCATACATCTGCAGGGAAATCTACGGGGCTGAGTCACCTGCACCAGCATAAAGTGATT
CATCGAGATATTAAAGGGAAAATGTCTGACTGAAAATGCAGAAGTTAAACTAGTGGACTTGGAGTCAGT
GCTCAGCTTGATCGAACAGTGGCAGGAGGAATACTTTCATGGAACCTCCTACTGGATGGCACCAGAAGTTATT
GCCTGTGATGAAAACCCAGATGCCACATATGATTCAAGAGTGACTTGTGGTCTTGGTATCACCGCCATTGAA
ATGGCAGAAGGTGCTCCCCCTCTGTGACATGCACCCATGAGAGCTCTCTTCATCCCCCGGAATCCAGCG
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CGGAGGGACTTCTGAGGCTGCAGCTGGCAACAAAGGAGCAGCTGAGGAGGAGCAGCTGGAGGAGCAGCTGGAGCAG
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AGAGCAAGCAACCTGATCTCGGAGAACTGAGCCCATCTGGAGAGGCCCTGAGGAGCAGCAGTGGCAGT
TCCTCCAGCTCCAGCACCCCTAGCTCCAGCCAGCTCCCAAGGAGGCTCCAGGCTGGATCACAAGCAGGATCC
AGTGAACGCACCAGAGTTGAGCCAACAGTAAGTCAGAAGGATCACCTGTGCTTCCCATGAGCCTGCCAGGTG
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TCCTCTCCAGTGAGGAGTCAGAAAGTAGCGAGGAAGAGGAGGAAGATGGAGAGAGCGAGACCCATGATGGGACA
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CGGTAGTGGAAACAGGACATTGGATGGAGTATTGATGATGAGCTAAAGGTTAAAGTTCTATGTGAA
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AATTCCATGATGAACCTGGTAA

Figure 23

ATGGCGAGCGACTCCCCGGCTCGAAGCCTGGATGAAATAGATCTCTCGGCTCTGAGGGACCCCTGCAGGGATCTT
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GCAGCCATCAAGGTTATGGATGTACAGGGGATGAAGAGGAAGAAATCAAACAAGAAATTACATGTTGAAGAAA
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CTTGTTGGTGTGGAGTTGTGCTGGCTCTGTCACCGACCTGATCAAGAACACAAAAGTAACACGTTG
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GCTCAGCTGATCGAACAGTGGCAGGAGGAATACTTCATGGAACCTCCTACTGGATGGCACCAGAAGTTATT
GCCTGTGATGAAAACCCAGATGCCACATATGATTCAAGAGTGACTTGTGGCTTGGTATCACCGCCATTGAA
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CCTCGGCTGAAGTCTAAGAAGTGGTCAAAAAAATTCCAGTCATTATTGAGAGCTGCTGGTAAAGAACATCACAGC
CAGCGACCAGCAACAGAACATTGATGAAGCATCCATTATACGAGACCAACCTAATGAGCGACAGGTCGCATT
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GTTTCCCTTCAGCATCAGCGGAGGAGCAGAGGCCCTGTGGAGAAGAACCCACTGTACCTTACAAAGAACAGGAATG
AGTCCTAGTGAGAACGCCAGCATGGCCAAGGAGATCCCACATCTGGTAGCTGAAAATCCCAGGGACCTGCCTTG
ACCGCCTCCAGTCAGTCAGCAGCAGGCCACAAAGGCCCTCTGGGTTTCAGGAGGCTCTGAACGTGACCTCC
CACCGCGTGGAGATGCCACGCCAGAACTCAGATCCCACCTGGAAAATCTCCTCTCCCCACTCGCATTGAAAAG
TTGACCGAAGCTTGGTTACGACAGGAAGAACATTCCACCAAAAGGTGCCTCAAAGAACAAACTCTATATCC
CCAGCATTAGCCAGAAAGAATTCTCTGGGAATGGTAGTGCTCTGGGACCCAGACTAGGATCTCAACCCATCAGA
GCAAGCAACCCCTGATCTCCGGAGAACTGAGCCATCTGGAGAGGCCCTTGAGAGGACCAGCAGTGGCAGTTCC
TCCAGCTCAGCACCCCTAGCTCCAGGCCAGCTCCAAAGGAGGCTCCAGCCTGGATCACAAGCAGGATCCAGT
GAACGCACCAAGAGTTGAGCCAACAGTAAGTCAGAAGGATCACCTGTGCTTCCCCATGAGCCTGCCAAGGTGAA
CCAGAAGAATCCAGGGACATTACCCGGCCAGTCAGCAGCTAGCTACAAAAAAGCTATAGATGAGGATCTGACG
GCATTAGCCAAGAAACTAAGAGAACTCCGGATTGAAGAAACAAACGCCCAATGAAGAAGGTGACTGATTACTCC
TCCTCCAGTGAGGAGTCAGAAAGTAGCGAGGAAGAGGAGGAAGATGGAGAGAGCGAGACCCATGATGGACAGTG
GCTGTCAGCGACATACCCAGACTGATACCAACAGGAGCTCAGGCAGCAACGAGCAGTACAATGTGGGAATGGT
GGGACGCATGGCTGGAGACCTCTCATCGGCAGCTTCAGCGCAGTATTCAGAGGACCATGCTGGGACTGATT
AGAGAGACGTCTGGAGAGAAGAGCGATCTGGCCACAGTGACAGCAATGGCTTGCTGGCACATCAACCTCCCT
GACCTGGTCAGCAGGCCATTCTCAGCTGGAAACCCGACTGAGGGACTGGGGCGCTCTCAACCCATTCCAG
GAGATGGACTCTGGGACTGAATATGGCATGGGAGCAGCACCAAAAGCCTCTCACCCCTTGAGGACCCAGA
GTATACCAGACGTCTCCACTGATGAAGATGAAGAGGATGAGGAATCATCGCCAGCTCTGTTACTAGCGAA
CTTCTTAGGCAAGAACAGGCCAAACTCAATGAAGCAAGAAAGATTGCGTGGTAAATGTAACCCAAACCAACATT
CGGCCTCATAGCGACACACCAGAAATCAGAAAATACAAGAACGATTCAACTCAGAAATACTTGTGAGCTCTG
TGGGTGTAACCTCTGGTGGGACTGAAAATGCCCTGATGCTTGGACCGAAGTGGCAAGGCAAAGTCTAT
AATCTGATCAACCGGAGGCAGTTCAGCAGATGGATGTGCTAGAGGACTGAATGTCCTTGACAAATTTCAGGA
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AAGAAACAAGGCTGGATCACTGTTGGGACTTGGAAAGGCTGTATACATTATAAGTGTAAATATGAAAGGATC
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CCATCTCATATTCAAGGGCAATATCACTCCTCATGCTATTGTCATCTGCCTAAACAGATGGAATGGAATGCTT
GTTGCTATGAGGATGAGGGGTGTATGAAACACCTATGGCCGGATAACTAAGGATGTGGCTCCAATGGGGA
GAAATGCCACGTCTGGCTACATTCCAATCAGATAATGGCTGGGCGAGAAAGCTATTGAGATCCGG
TCAGTGGAAACAGGACATTGGATGGAGTATTGATGATAAGCGAGCTCAAAGGTTAAAGTGTATGAAAGA
AATGATAAGGTATTTTGATCCGTGCGATCTGGAGGAAGTAGCCAAGTGTGTTTATGACCCCTAACAGAAAT
TCCATGATGAACTGGTAA

Figure 24

ATGGCGAGCGACTCCCCGGCTCGAAGCCTGGATGAAATAGATCTCTCGGCTTGAGGGACCCCTGCAGGGATCTT
GAATTGGTGGAACTTGTGGAAATGGAACATAACGGGCAAGTTATAAGGGTCGTATGTCAAAACGGGCCAGCTT
GCAGCCATCAAGGTTATGGATGTACAGGGGATGAAGAGGAAGAAATCAAACAAGAAATTAAACATGTTGAAGAAA
TATTCTCATCACCGGAATATTGCTACATACATGGTCTTTATCAAAGAACCCACCAGGCATGGATGACCAA
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GCCTGTATGAAAACCCAGATGCCACATATGATTCAAGAGTGACTTGTGGTCTTGGTATCACCGCCATTGAA
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CAGCGACCAGCAACAGAACATTGATGAAGCATCCATTATACGAGACCAACCTAATGAGCGACAGGTCCGCATT
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CGGAGGGACTTCTGAGGCTGAGCTGCCAACAGGAGCAGCTGAGGAGGAGGAGGAGGAGGAGCAGCTGGAGCAG
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GTTCAAGCTGCTCGAACACCCCCCATGCTCAGACAGTCAGTCCCAGATCCCACATCTGGTAGCTGTAAAATCC
CAGGGACCTGCCTGACCGCCTCCAGTCAGTGACAGCAGCCCACAAAGGCCTCTCTGGGTTTCAGGAGGCT
CTGAACGTGACCTCCCACCGCGTGGAGATGCCACGCCAGACTCAGATCCCACCTCGGAAAATCCTCTCT
ACTCGCATTGAAAAGTTGACCGAAGCTTGGTTACGACAGGAAGAACATCCACCAAGGTGCCCTAAAGA
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CAAGCAGGATCCAGTGAACGCACCAGAGTTCGAGCCAACAGTAAGTCAGAAGGATCACCTGTGCT
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ACAGGACATTGGATGGAGTATTGATGCTAGGAGGAGTAGCCAAGTGT
GTATTGTTGCATCGTGCATGGAGGAGTAGCCAAGTGT
AACTGGTAA

Figure 25

ATGGCGAGCGACTCCCCGGCTCGAAGCCTGGATGAAATAGATCTCTGGCTCTGAGGGACCTGCAGGGATCTT
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GGACATTGGATGGAGTATTATGCATAAGCGAGCTAAAGGTTAAAGTTCTATGTAAGAACATGATAAGGTA
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TGGTAA

Figure 26

ATGGCGAGCGACTCCCCGGCTCGAAGCCTGGATGAAATAGATCTCTGGCTCTGAGGGACCTGCAGGGATCTT
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CGGAGGGACTTCTGAGGCTGAGCTGGCAACAAGGAGCAGTTCTGAGGCCCTACGGAGGCAGCAGCTGGAGCAG
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CGAACACCCCCCATGCTCAGACCAGTCGATCCCCAGATCCACATCTGGTAGCTGAAAATCCCAGGGACCTGCC
TTGACCGCTCCAGTCAGTGCACGAGCAGCCCACAAGGGCCTCTGGGTTTCAGGAGGCTCTGAAACGTGACC
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GATGAAGATGAAAGAGGATGAGGAATCATCAGCCGAGCTCTGTTACTAGCGAACTCTTAGGCAAGAACAGGCC
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GAAATCAGAAAATACAAGAACGATTCAACTCAGAAATACTTGTGCAGCTGTGGGTTGAAACCTTCTGGT
GGGACTGAAAATGGCCTGATGCTTGGACCGAAGTGGCAAGGCAAAGTCTATAATCTGATCAACCGGAGGCCA
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GTGTATGTAACACCTATGGCGGATAACTAAGGATGTGGTGTCCAATGGGAGAACAGCTATTGAGATCCGGTCA
GAGTGGAAACAGGACATTGAGTGGTAAAGGTTCTATGTGAAAGAACAGGACATTG
TCCGTGCATCTGGAGGAAGTAGCCAAGTGTGTTCATGACCTCAACAGAAATTCCATGATGAACTGGTAA>

Figure 27

ATGGCGAGCGACTCCCCGGCTCGAAGCCTGGATGAAATAGATCTCTCGGCTTGAGGGACCTGCAGGGATCTT
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CACCGCGTGGAGATGCCACGCCAGACTCAGATCCCACCTCGAAAATCCTCCTCTCCCACTCGCATTGAAAAG
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TATGTAACACCTATGGCGGATAACTAAGGATGTGGTGCTCCAATGGGAGAAATGCCACGTCTGGCCTAC
ATTCAATTCAACAGATAATGGCTGGGGCGAGAAAGCTATTGAGATCCGGTCAGTGGAAACAGGACATTGGAT
GGAGTATTGATGCTAAAGGTTAAAGTTCTATGTAAGAACAAATGATAAGGTATTTTGATCC
GTGCGATCTGGAGGAAGTAGCCAAGTGTGTTCATGACCTCAACAGAAATTCCATGATGAACGGTAA

Figure 28

ATGGCGAGCGACTCCCCGGCTCGAAGCCTGGATGAAATAGATCTCTCGGCTCTGAGGGACCCCTGCAGGGATCTT
GAATTGGTGGAACTTGTGGAAATGGAACATACGGGCAAGTTATAAGGGTCGTATGTCAAACAGGGCCAGCTT
GCAGCCATCAAGGTTATGGATGTCACAGGGATGAAGAGGAAGAAATCAAACAAGAAATTAAACATGTTGAAGAAA
TATTCTCATCACCGGAATATTGCTACATACATGGTCTTATCAAAAAGAACCCACCAGGCATGGATGACCAA
CTTGGTGGTGTATGGAGTTGTGGTCTGGCTCTGCACCGACCTGATCAAGAACACAAAAGGTAAACACGTTG
AAAGAGGAGTGGATTGCATACATCTGCAGGGAAATCTTACGGGGCTGAGTCACCTGCACCAGCATAAAGTGATT
CATCGAGATATTAAAGGGCAAATGTCTGACTGAAAATGCAGAAGTAAACTAGTGGACTTGGAGTCAGT
GCTCAGCTTGATCGAACAGTGGCAGGGAGGAATACCTTCATGGAACCTCCTACTGGATGCCACCAGAACGTTATT
GCCTGTGATGAAAACCCAGATGCCACATATGATTCAAGAGTGACTTGTGGCTTGGTATCACCGCATTGAA
ATGGCAGAAGGTGCTCCCCCTCTGTGACATGCACCCCCTGAGAGCTCTCTCATCCCCCGGAATCCAGCG
CCTCGGCTGAAGTCTAAGAAGTGGTCAAAAAAATTCCAGTCATTATTGAGAGCTGCTGGTAAAGAACACAGC
CAGCGACCAGCAACAGAACATTGATGAAGCATCCATTATCAGAGACCAACCTAATGAGCAGACAGGTCCGCATT
CAACTCAAGGACCATATTGATAGAACAAAGAAGAAGCGAGGAGAAAAGATGAGACAGAGTATGAGTACAGTGG
AGTGAGGAAGAAGAGGAGGAATGACTCAGGAGAGCCAGCTCATCCTGAATCTGCCAGGGAGTCAGCCTG
CGGAGGGACTTCTGAGGCTGCAGCTGGCAACAAGGAGCCTTGAGGGCCCTACGGAGGCAGCTGGAGCAG
CAGCAGCGGAGAATGAGGAGCACAAGCGCAGCTGCTGGCGAGCGTCAGAACGCATCGAGGAGCAGAAAGAG
CAGAGCGCGGCTGGAGGAGCAACAAAGGCAGAGAGAAGGGAGCTGCGGAAGCAGCAGGAGAGGGAGCAGCGCG
CACTATGAGGAGCAGATGCGCCGGAGGAGGAGGAGGAGCAGTCAGAACAGGAATATAAGCGCAAACAA
TTGGAAGAACAGAGAACAGAACAGAACAGACTGCAGAGGCAGCTAACAGCAAGAACAGAGACTACTTAGTTCCCTCAG
CATCAGCGCAGGAGCAGAGGCCCTGTGGAGAACAGGAAAGCCACTGTACCATTAACAAAGAACAGGATGAGTCTAGTGAG
AAGCCAGCATGGCCAAGGAGATCCCACATCTGGTAGCTGTAATCCAGGGACCTGCCTTGACCGCCTCCAG
TCAGTGCACGAGCAGCCCACAAAGGGCTCTCTGGTTCAAGGAGGCTCTGAACGTGACCTCCACCGCTGGAG
ATGCCACGCCAGAACCTCAGATCCCACCTCGAAAATCCTCTCCCCACTCGCATTGAAAAGTTGACCGAAC
TCTTGGTTACGACAGGAAGAACAGACATTCCACAAAGGTGCCTCAAAGAACAACTCTATATCCCCAGCATTAGCC
AGAAAGAATTCTCCTGGGAATGGTAGTGTCTGGACCCAGACTAGGATCTAACCCATCAGAGCAAGAACCC
GATCTCCGGAGAACCTGAGCCCATCTGGAGAGGCCCTTGAGAGGACCAGCAGTGGCAGTCTCCAGCTCCAGC
ACCCCTAGCTCCAGCCCAGCTCCAAGGAGGCTCCAGCCTGGATCACAAGCAGGATCCAGTGAACGCACCAGA
GTTCGAGCCAACAGTAAGTCAGAAGGATCACCTGTGCTTCCCATGAGCCTGCAAGGTGAAACCAGAACAG
AGGGACATTACCCGGCCAGTCGACCAGCTGATCTGACGGCATTAGCAAAGAACAGAACACTCCGGATTGAA
GAAACAAACCGCCCAATGAAGAACGGTACTGATTACTCCTCTCCAGTGAGGAGTCAGAAAGTAGCGAGGAAGAG
GAGGAAGATGGAGAGAGCAGACCCATGATGGACAGTGGCTGTCAAGCAGATACCCAGACTGATACCAACAGGA
GCTCCAGGCAGCAACGAGCAGTACAATGTGGGAATGGTGGGACGCATGGCTGGAGACCTCTCATGGGACAGT
TTCAGCGGAGTATTCAAGAACAGGAACTTGATGATTAGAGAGACGTCTGGAGAGAACAGCAGTCTGGC
AGTACAGCAATGGCTTGCTGGCACATCAACCTCCCTGACCTGGCAGCAGAGCCATTCTCAGCTGGAAC
CCGACTGAGGGACTGGGCGCGTCTAACCCATTCCAGGAGATGGACTCTGGACTGAAATATGGCATGGGAGC
AGCACCAAAAGCCTCTCACCCCTTGTGGACCCAGAGTATACCAGACGTCTCCACTGATGAAGATGAAGAG
GATGAGGAATCATCAGCGCAGCTCTTTACTAGCGAACTCTTAGGCAAGAACAGGCCAAACTCAATGAAGCA
AGAAAGATTGGTGGTAAATGTAACCAACATTGCCCTCATAGCGACACACCAGAAATCAGAAAATAC
AAGAACGATTCAACTCAGAAATACCTTGTGCAGCTGTGGGTGAAACCTCTGGTGGGACTGAAATGGC
CTGATGCTTGGACCGAAGTGGCAAGGCAAAGTCTATAATCTGATCAACCGGAGGCATTTCAGCAGATGGAT
GTGCTAGAGGGACTGAATGCTTGTGACAATTTCAGGAAAGAACAGTACGAGTTACTATCTTGT
TTAAGAAACAGAACATACATAATGACCCAGAACAGTAGAAAAGAACAGGCTGGATCACTGTTGGGACTTGGAA
GGCTGTATACATTATAAAGTTGTTAAATATGAAAGGATCAAATTGGTGTGATTGCCTTAAAGAACAGTGTGGAA
ATATATGCTTGGCTCCTAAACCGTATCATAAATTGATGCAACCTGAGCTTGTGAGATCTCCAGCACAGC
CTGCTAGTTGATCTACGGTAGAACAGGTAAGGTTATTGGTGTGACACACTGGTTCCATGTA
ATTGATGTTGATTCAAGGAAACTCTTATGATATCTACATACCATCTCATATTCAAGGCAATATCACTCCTCATGCT
ATTGTCATCTGCCTAAACAGATGGAATGGAATGCTTGTGCTATGAGGATGAGGGGTGTATGAAACACC
TATGGCCGGATAACTAAGGATGTGGCTCCAATGGGAGAACAGGCCACGTCTGGCCTACATTCAATT
CAGATAATGGCTGGGCGAGAACAGCTATTGAGATCCGGTCAGTGGAAACAGGACATTGGATGGAGTATTATG
CATAGCGAGCTCAAAGGTTAAAGTTCTATGTGAAAGAACAGTAAAGGTATTTTGCACTCCGTGCGATCTGGA
GGAAGTAGCCAAGTGTGTTCATGACCCCTCAACAGAAATTCCATGATGAACGGTAA

Figure 29

1 MASDSPARSLDEIDL SALRD PAGIFEL VELVGNGTYGQVYKGRHVKTGQLAAIKVMDVTG
61 DEEEEIKQEINMLKKYSHHRNIATYYGAFIKKNPPGMDDQLWLVMFCGAGSVTDLIKNT
121 KGNTLKEEWIAIYC REILRGLSHLHQHKVIHRI DIKGQNVL TENAEVKLVDGFVSAQLDR
181 TVGRRNFTIGTPYWM APEVIA CDENPD ATYDFKSDLW S L GITAI EMAEGAPPLCDMHPMR
241 ALFLIPRNPA PRLKS KKW SKKF QSFIESCLVKNHSQR PATEQLMKH PFI RDQP NERQVR I
301 QLKDHIDRTKKRGEKDET EYEYSGSEEEENDSGEPSSILNLPGESTLRRDFLRLQLA
361 NKERSEALRRQQLEQQQRENEEHKRQLLAERQKRIEEQKEQRRRLEEQQRREKELRKQQE
421 REQRRHYEEQMREEERRRAEHEQEYKRQLEEQRQAERLQRQLKQERDYLVLQHQRQE
481 QRPVEKKPLYHYKEGMS PSEKPA WAKEVEERSRLNRQSS PAMPHKVANRISDPNLPPRSE
541 SFSISGVQPARTPPMLRPVDPQI PHLVAVKSQGPALTASQSVHEQPTKGLSGFQEALNVT
601 SHRVEMPRQNSDPTSEN PPLPTRIEKFDRSSWLRQ EEDIPP KVPQRTTSISP ALARKNSP
661 GNGSALGPRLGSQPIRASN PDLR RT EPILESPLQRTSSGSSSSSTPSSQPSSQGSQPG
721 SQAGSSERTRVRANSKSEGSPVLPHEPAVKPEESRDITRPSRPASYKKA IDEDLTALAK
781 ELRELRIEETN RPMKKVTDYSSSEESSEEEEDGESETHDGTAVSDIPRLI PTGAP
841 GSNEQYNVGMVGTHGLETSHADSFSGSISREGTLMIRETSGEKKRSGHSDSNGFAGHINL
901 PDLVQQSHSPAGTPTEGLGRVSTHSQEMDSGTIEYGMGSSTKASFTPFDPRVYQTSP TDE
961 DEEDEESSAAALFTSELLRQEQA KLNEARKISVVNVNPTNIRPHSDTPEIRKYKKRFNSE
1021 ILCAALWGVNLLVGTE NGMLLDRSGQGKVNLI INRRRFQ QMDVLEG NVLVTISGKKNK
1081 LRVYYLSWLRN RILHNDPEVEKKQGWITVGDLEG CIHYKVVKYERIKFLVIALKNAVEIY
1141 AWAPKPYHKFMAFKSFADIQHKPLLVDLTVEEGQRLKVI FGSHTGFHVIDV DSGNSYDIY
1201 IPSHIQGNITPHAI VILPKTDGMEMLV CYEDEGVYVNTYGRITKD VVLQWGEMPTSVAYI
1261 HSNQIMGWGEKAIEIRS VETGHLDGVFMHKRAQRLKFL CERNDKVFFASVRSGGSSQVFF
1321 MTLNRNSMMNWZ

Figure 30

1 MASDSPARSLDEIDL SALRDPAGIFELVELVGNGTYGQVYKGRHVKTGQLAAIKVMDVTG
61 DEEEEIKQEINMLKKYSHIRNIATYYGAFIKKNPPGMDDQLWLVMFCGAGSVTDLIKNT
121 KGNTLKEEWIAYICREILRGLSHLHQHKVIHRDIKGQNVLLENAEVKLVDFGVSAQLDR
181 TVGRRNFTIGTPYWMAP EVIACDENPDATYDFKSDLWLSLGITAIEMAEGAPPLCDMHPMR
241 ALFLIPRNPA PRLKS KWSKKFQS FIESCLVKNHSQR PATEQLMKH PFIRDQPNERQVRI
301 QLKDHIDRTKKKRGEKDET EYEYSGSEEEENDSGEPSSILNLPGESTLRRDFLRLQLA
361 NKERSEALRRQQLEQQQRENEEHKRQLLAERQKRIEEQKEQRRLLEEQQRREKELRKQQE
421 REQRRHYEEQMREEERRRAEHEQEYIRRQLEEEQRQLEILQQQLLHEQALLLEYKRKQL
481 EEQRQAERLQRQLKQERDYL VSLQHQRQEQR PVEKKPLYHYKEGMSPSEKPAWAKEIPH
541 VAVKSQGPALTASQSVHEQPTKGLSGFQEALNVTSHRVEMPRQNSDPTSENPLP TRIEK
601 FDRSSWLRQEE DIPP KVPQRTT SISPALARKNS PGNGS ALG PRLGSQPI RASNPDLR RT
661 PILESPLQRTSSGSSSSSTPSSQPSQGGSQPGSQAGSSERTRVRANSKSEGSPVLPHE
721 PAKVKPEESRDITRPSRPASYKKAIDEDLTALAKELRELRIEETNRPMKKVTDYSSSSEE
781 SESSEEEEDGESETHDGTVAVSDIPRLIPTGAPGSNEQYNVGMVGTHGETSHADS FSG
841 SISREGTL MIRETSGEKKRSGHSDNSNGFAGHINLPDLVQQSHSPAGTPTEGLGRVSTHSQ
901 EMDSGTEYGMGSSTKASFTPFDPRVYQTSP TDEDEEDEESSAAALFTSELLRQEQA KLN
961 EARKISVVNVNPTNIRPHSDTPEIRKYKKRFNSEILCAALWGVNLLVGTEENGLMLDRSG
1021 QGKVYNL LINRRRFQ QMDVLEG NVL VTISGKKNKLRVYYLSWLRNRI LHDNPEVEKKQGW
1081 ITVG DLEGCIHYKVVKYERIKFLVIALKNAV EYI A WAPKPYHKFM AFKS FADLQHKPLL
1141 DLTVEEGQRLK VIFGSHTGFHVIDV DSGNSYDIYI PSHI QGNITPHAI VILPKTDGMEML
1201 VC YED EG VVNTYGRITKD VV LQW GEMPTSVAYIHSNQIMWG EKAIEIRS VETGHLDGV
1261 FMHKRAQRLKFL CERND KVFFASVRSGGSSQVFFMTLN RNSMMNWZ

Figure 31

1 MASDSPARSLDEIDL SALRDPAGIFELVELVGNGTYGQVYKGRHVKTGQLAAIKVMDVTG
61 DEEEEIKQEINMLKKYSHHNIATYYGAFIKKNPPGMDDQLWLVMFCGAGSVTDLIKNT
121 KGNTLKEEWIAYICREILRGLSHLHQHKVIHRDIKGQNVLLTENAEVKLVDFGVSAQLDR
181 TVGRRNTFIGTPYWMAPPEVIACDENPDATYDFKSDLWLSLGITAIEMAEGAPPLCDMHPMR
241 ALFLIPRNPAAPRLKSKKWSKKFQSFIESTCLVKNHSQRPATEQLMKHPFIRDQPNERQVRI
301 QLKDHIDRTKKRKGEKDET EYEYSGSEEEEEENDSGEPSSILNLPGESTLRRDFLRLQLA
361 NKERSEALRRQQLEQQQRENEEHKRQLLAERQKRIEEQKEQRRRLEEQQRREKELRKQQE
421 REQRRHYEEQMREEERRRAEHEQEYIRRQLEEEQRQLEILQQQLLHEQALLLEYKRKQL
481 EEQRQAERLQRQLKQERDYLVSLQHQRQEQRPVKEKKPLYHYKEGMSPSEKPAWAKEVEER
541 SRLNRQSSPAMPHKVANRISDPNLPPRSESFSISGVQPARTPPMLRPVDPQIPIHLVAVKS
601 QGPALTASQSVHEQPTKGLSGFQEALNVTSHRVEEMPRQNSDPTSENPPLPTRIEKFDRSS
661 WLRQEEDIPPKVQRTTSISPALARKNSPGNGSALGPRLGSQPIRASNPDLLRTEPILES
721 PLQRTSSGSSSSSTPSSQPGSQAGSSERTRVRANSKSEGSPVLPHEPAKVK
781 PEESRDITRPSRPADLTALAKELRELRIETNRPMKKVTDYSSSESESSEEEEDGES
841 ETHDGTAVAVSDIPRLIPTGAPGSNEQYNVGMVGHLETSHADSFGSISREGTLMIRET
901 SGEKKRSGHSDSNGFAGHINLPDLVQQSHSPAGTPTEGLGRVSTHSQEMDSGTEYGMGSS
961 TKASFTPVFDPRVYQTSPTEDEDEEDEESSAALFTSELLRQEQAQLNEARKISVVNVNPT
1021 NIRPHSDTPEIRKYKKRFNSEILCAALWGVNLLVGTENGLMLLDRSGQGKVNLYLINRRF
1081 QQMDVLEGLNVLVTISGKKNKLRYYLSWLRNRILHNDPEVEKKQGWITVGDLEGCIHYK
1141 VVKYERIKFLVIALKNAVEIYAWAPKPYHKFMFKSFADLQHKPLLVDLTVEEGQRLKVI
1201 FGSHTGFVIDVDSGNSYDIYIPSHIQGNITPHAIIVILPKTDGMEMILVCYEDEGVYVNTY
1261 GRITKDVLQWGEMPTS VAYIHSNQIMGWEKAIEIRS VETGHLDGVFMHKRAQLKFLC
1321 ERNDKVFASVRSGGSSQFFMTLNRSMMNWZ

Figure 32

1 MASDSPARSLDEIDL SALRDPAGIFELVELVGNGTYGQVYKGRHVKTGQLAAIKVMDVTG
61 DEEEEIKQEINMLKKYSHH RNIATYYGAFIKKNPPGMDDQLWLVMFCGAGSVTDLIKNT
121 KGNTLKEEWIAYICREILRGLSHLHQHKVIHRDIKGQNVL TENAEVKLVDGFVSAQLDR
181 TVGRRNFTIGTPYWMAPEVIACDENPDATYDFKSDLWSLGITAIEMAEGAPPLCDMHPMR
241 ALFLIPRNPA PRLKSKKW SKKFQSFI ECLVKNHSQR PATEQLMKHPFIRDQPNERQVR I
301 QLKDHIDRTKKRGEKDET EYEYSGSEEEENDS GEPSSILNLPGE STLRRDFLRLQLA
361 NKERSEALRRQQLEQQQRENEEHKRQLLAERQKRIEEQKEQRRRLEEQQRREKELRKQQE
421 REQRRHYEEQMREEERRRAEHEQEYKRQLEEQRQAERLQRQLKQERDYLVSLQHQRQE
481 QRPVEKKPLYHYKEGMS PSEKPAWAKEIPLHVAVKSQGPALTASQSVHEQPTKGLSGFQE
541 ALNVTSHRVEMPRQN SDPTSEN PPLPTRIEKFDRSSWLQEE DIPP KVPQRTTSISPALA
601 RKNSPGNGS ALGPRLGSQP IRASNPDLRTEPILESPLQ RTSSGSSSSSTPSSQPSSQG
661 GSQPGSQAGSSERTRV RANSKSEGS PVL PHEPA KVPEESRDITRPSRPASYKKA IDEDL
721 TALAKELRELRIEETNRP MKVTDYSSSSE ESESSEEEEDGESETHDGTVAVSDIPRLI
781 PTGAPGSNEQYNVGMVGTHGLETS HADSFGSI SREGTLMI RETSGEKKRSGHSDSNGFA
841 GHINLPDLVQOSHSPAGTPTEGLGRVSTHSQEMDSGTEYGMGSSTKASFTP FVDPRVYQT
901 SPTDEDEDEESSA AALFTSELLRQEQA KLNEAR KISVVNVNPTNIRPHSDTPEIRKYKK
961 RFNSEILCAALWGVNLLVG TENG LMLLDRSGQGKVYNL INRRRFQ QMDVLEG LNVLVTIS
1021 GKKNKL RVYYLSWLRNRILHNDPEVEKKQGWITVGDLEG CIHYKVVKYERIKFLVIALKN
1081 AVEIYAWAPKPYHKFMAFKSFADLQHKPLLVDLTVEEGQRLK VIFGSHTGFH IDVDSGN
1141 SYDIYIPSHIQGNITPHAI VILPKTDGMEMLV CYEDEGVVNTYGRITKD VVLQWGEMPT
1201 SVAYIHSNQIMWGGEKAIEIRSVETGHLDGVFMHKRAQRLKFLCERN DKVFFASVRSGGS
1261 SQVFFMTLN RNSMMNWZ

Figure 33

1 MASDSPARSIDLSALRDPAGIFELVELVGNQTYGQVYKGRHVKTGQLAAIKVMDVTG
61 DEEEEIKQEINMLKKYSHRNIAATYYGAFIKNPPGMDDQLWLVMFCGAGSVTDLIKNT
121 KGNTLKEEWIAYICREILRGLSHLHQHKVIHRDIKGQNVLLTENAEVKLVDFGVSAQLDR
181 TVGRRNTFIGTPYWMAPEVIACDENPDATYDFKSDLWSLGITATEMAEGAPPLCDMHPMR
241 ALFLIPRNPAPRLKSKKWKKFQSFIESTCLVKNHSQRPAEQLMKHPFIRDQPNERQVRI
301 QLKDHIDRTKKRGEKDETLEYSGSEEEENDSGEPSILNLPGESTLRRDFLRLQLA
361 NKERSEALRRQQLEQQQRENEEHKRQLLAERQKRIEEQKEQRRRLEEQQRREKELRKQQE
421 REQRRHYEEQMREEERRRAEHEQEYKRQLEEFQRQAERLQRQLKQERDYLVSQHQRQE
481 QRPVEKKPLYHYKEGMSPSEKPAWAKEVEERSRLNRQSSPAMPHKVANRISDPNLPPRSE
541 SFSISGVQPARTPPMLRPVDPQIPLHLVAVKSQGPALTASQSVHEQPTKGLSGFQEALNVT
601 SHRVEMPRQNNSDPTSENPLPTRIEKFDRSSWRQEEDEIPPKVVPQRTTSISPALARKNSP
661 GNGSALGPRLGSQPIRASNPDLRRTEPILESPLQRTSSGSSSSSTPSSQPSQGSQPG
721 SQAGSSERTRVRANSKSEGPVLPHEPAVKPEESRDITRPSRPADLTALAKELRELRIE
781 ETNRPMMKVTDYSSSEESSEEEEDGESETHDGTVAVDIPLIPTGAPGSNEQYNV
841 GMVGTHGLETSHADSFGSISREGTLMIRETSGEKKRSGHSDNSNGFAGHINLPDLVQQSH
901 SPAGTPTEGLGRVSTHSQEMDSGTEYGMGSSTKASFTPFDPRVYQTSPPTDEDEDEESS
961 AAALFTSELLRQEQAQLNEARKISVVNVNPTNIRPHSDTPEIRKYKKRFNSEILCAALWG
1021 VNLLVGTENGMLLDRSQGKQVYNLINRRRFQQMDVLEGNLVLTISGKKNKLRYYLSW
1081 LRNRILHNDPEVEKKQGWITVGDLEGCIHYKVVKYERIKFLVIALKNAVEIYAWAPKPYH
1141 KFMAFKSFADLQHKPLLVDLTVEEGQRLKVIFGSHTGFVIDVDSGNSYDIYIPSHIQGN
1201 ITPHAIVILPKTDGMEMLVCYEDEGVYVNTYGRITKDVLQWGEMPTSVAIHSNQIMGW
1261 GEKAIEIRSVEVGHLDGVFMHKRAQRALKFLCERNDKVFFASVRSGGSSQVFMTLNRSNM
1321 MNWZ

Figure 34

1 MASDSPARSLDEIDL SALRDPAGIFELVELVGN GTYGQVYKGRHVKTGQLAAIKVMDVTG
61 DEEEEIKQEINMLKKYSHH RNIATYYGAFIKKNPPGMDDQLWLVMFCGAGSVTDL I KNT
121 KGNTLKEEWIAYICREILRGLSHLHQHKVIHRIKGQNVLLTENAEVKLVD FGVSAQLDR
181 TVGRRNTFIGTPYWM APEVIACDENPDATYDFKSDLWLSLGITAIEMAEGAPPLCDMHPMR
241 ALFLIPRNPA PRLKSKKWSKKFQS FIESCLVKNHSQR PATEQLMKHPFIRDQPNERQVR I
301 QLKDHIDRTKKKRGEKDET EYEYSGSEEEEEEENDSGEPSSILNLPGESTLRRDFLRLQLA
361 NKERSEALRRQQLEQQQRENEEHKRQ LLAERQKR IEEQKEQRRRLEEQQRREKELRKQQE
421 REQRRHYEEQM RREEERRRAEHEQ EYIRRQLEEEQRQLEILQQQLLHEQALLLEYKRKQL
481 EEQRQAERLQRQLKQERDYL VSLQHQ RQEQRPVEKKPLYHYKEGMS PSEKPAWAKEI PHL
541 VAVKSQGPALTASQSVHEQPTKGLSGFQEALNVTSHRVEMPRQNSDPTSEN PPLP TRIEK
601 FDRSSWLRQEE DIPP KVPQRTTSISP ALARKNSPGNGS ALGP RLGS QPIRASNPDL RRTE
661 PILESPLQRTSSGSSSSSTPSSQPSQGGSQPGSQAGSSERTRVRANSKSEGSPVLPHE
721 PAKVKPEESRDITRPSRPADLTALAKELRELRIETNRPMKKVTDYSSSEESSEEEE
781 EDGESETHDGTVA VSDIPRLIPTGAPGSNEQYNVGMVGTHGLE TSHADS FSGSISREGTL
841 MIRETSGEKKRSGHS DSNGFAGHINLPDLVQQSHSPAGTPT EGLGRVSTHSQEMDSGTEY
901 GMGSSTKASFTP FVDPRVYQT SPTDEDEEDEESSA AALFTSELLRQEQAKLNEARKISVV
961 NVNPTNIRPHSDTPEIRKYKKRFNSEI LCAALWGVNLLVG TENGMLLD RSGQGKVYNLI
1021 NRRRFQQMDVLEG LNVLVTISGKKNKL RVY YLSWLRN RILHNDPEVEKKQGWITVGDLEG
1081 CIHYKVV KYERIKFLVIA LKNAVEIYAWAPKPYHKFM AFKS FADLQHKPLLVDLTVEEGQ
1141 RLKVIFGSHTGF VIDVDS GNSYDIYI PSHIQGNITPHAI VILPKTDGMEMLV CYEDEGV
1201 YVN TYGRITKD VV LQWGEMPTSVAYIH SNQIM GWGEKAIEIR SVETGH LDGV FMHKRAQR
1261 LKFLCERNDK VFFASVRSGGSSQVFFMTLN RNSMMNWZ

Figure 35

1 MASDSPARSIDLSALRDPAGIFELVELVGNNTYGQVYKGRHVKTGQLAAIKVMDVTG
61 DEEEEIKQEINMLKKYSHHRNIATYYGAFIKKNPPGMDDQLWLVMFCGAGSVTDLIKNT
121 KGNTLKEEWIAYICREILRGLSHLHQHKVIHRDIKGQNVLLTENAEVKLVDFGVSAQLDR
181 TVGRRNTFIGTPYWMAPEVIACDENPDATYDFKSDLWSL GITAIEMAEGAPPLCDMHPMR
241 ALFLIPRNPAAPRLKSKKWSKKFQSFIESTCLVKNHSQR PATEQLMKHPFIRDQPNERQVRI
301 QLKDHIDRTKKKRGEKDETEYEYSGSEEEENDSGEPSSILNLPGESTLRRDFLRLQLA
361 NKERSEALRRQQLEQQQRENEEHKRQLLAERQKRIEEQKEQRRRLEEQQRREKELRKQQE
421 REQRRHYEEQMREEERRAEEHEQEYKRKQLEEQRQAERLQRQLKQERDYLVS LQHQRQE
481 QRPVEKKPLYHYKEGMSPSEKPAWAKEIPHLVAVKSQGPALTASQSVHEQPTKGLSGFQE
541 ALNVTSRHRVEMPRQNSDPTSENPLP TRIEKFDRSSWLRQEDIPPKVVPQRTTSISPALA
601 RKNSPGNGSALGPRLGSQPIRASNPDLLRTEPILESPLQRTSSGSSSSSTPSSQPSQG
661 GSQPGSQAGSSERTVRANSKSEGSPVLPHEPAVKPEESRDITRSPRPADLTALAKELR
721 ELRIEETNRPMKKVTDYSSSSEESSEEEEDGESETHDGTVAVSDIPLRIPTGAPGSN
781 EQYNVGMVGTHGLETSDFSISREGTLMIRETSGEKKRSGHSDSNGFAGHINLPDL
841 VQQSHSPAGTPTEGLGRVSTHSQEMDSGTEYGMGSSTKASFTPFDPRVYQTSPTEDEEE
901 DEESSAAALFTSELLRQEAKLNNEAR KISVVNVNPTNIRPHSDTPEIRKYKKRFNSEILC
961 AALWGVNLLVGTENGLMLDRSGQGKVYNLINRRRFQQMDVLEGNLVLTISGKKNKL RV
1021 YYLSWLRNRILHNDPEVEKKQGWITVGDLEGCIHYKVVKYERIKFLVIALKNAV EYAWA
1081 PKPYHKFMFKSFADLQHKPLLVDLTVEEGQRLKVIFGSHTGFHVIDVDGSNSYDIYIPS
1141 HIQGNITPHAIIVILPKTDGMEMLV CYEDEGVYVNTYGRITKDVLQWGEMPTS VAYIHSN
1201 QIMGWGEKAIEIRS VETGHLDGVFMHKRAQRKFL CERNDKVFFASVRSGGSSQVFFMTL
1261 NRNSMMNWZ